

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 3, 2005, 01:56:21 ; Search time 4713 Seconds
(without alignments)
4318.097 Million cell updates/sec

Title: US-10-735-256-2
Perfect score: 2226
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....LSAGLPSPLLCLLLLVPPhL 420

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	2130	95.7	1263	6	AX751537 Sequence
	6	2130	95.7	1304	10	AF532860 Rattus no
	7	2118	95.1	1263	10	AY250220 Mus muscu
	8	1866.5	83.8	1075	6	CQ728617 Sequence
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	13	1342.5	60.3	187566	2	AC015685 Homo sapi
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c	15	1280	57.5	236864	2	AC096003 Rattus no
	16	1272.5	57.2	196786	2	AC102636 Mus muscu
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	19	999.5	44.9	1486	5	AY263334 Danio rer
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	21	966.5	43.4	163986	2	CR812832 Danio rer
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	27	948	42.6	1326	9	AY250219 Homo sapi
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	34	931.5	41.8	3509	5	AY263333 Danio rer
	35	921	41.4	209782	10	AL603905 Mouse DNA
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	39	916	41.2	1338	10	AY250218 Mus muscu
	40	916	41.2	2681	10	BC030471 Mus muscu
c	41	910.5	40.9	194424	2	AC146871 Xenopus t
	42	837.5	37.6	1176	6	AX411541 Sequence
	43	826	37.1	157732	2	AC099825 Papio ham

AC092532 Papio anu
AC007663 Homo sapi

ALIGNMENTS

RESULT 1

AX411529

LOCUS	AX411529	1260 bp	DNA	linear	PAT 14-JUN-2002
-------	----------	---------	-----	--------	-----------------

DEFINITION Sequence 1 from Patent WO0229059.

ACCESSION AX411529

VERSION AX411529.1 GI:21444134

KEYWORDS

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Sah, D.W.Y., Cate, R.L. and Strittmatter, S.M.

TITLE Nogo receptor homologs

JOURNAL Patent: WO 0229059-A 1 11-APR-2002;

BIOGEN INC (US)

FEATURES

Location/Qualifiers

source

1. .1260

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/organism="Homo sapiens"
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/mol type="unassigned DNA"
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/db xref="taxon:9606"
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ORIGIN

Alignment Scores:

Pred. No.: 1.89e-105 Length: 1260

Score: 2226.00 Matches: 420

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
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DB: 6 Gaps: 0

US-10-735-256-2 (1-420) x AX411529 (1-1260)

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Db 61 CTCCTGGCCCTGCCCTGGCGGCCCCCAGCTGCCCCATGCTCTGCACCTGCTACTCATCC 120

Qy 41 ProProThrValSerCysGlnAlaAsnAsnPheSerSerValProLeuSerLeuProPro 60
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Db 121 CCGCCACCGTGAGCTGCCAGGCCAACAACTTCTCCTCTGTGCCGCTGTCCCTGCCACCC 180

Qy 61 SerThrGlnArgLeuPheLeuGlnAsnAsnLeuIleArgThrLeuArgProGlyThrPhe 80
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Db 181 AGCACTCAGCGACTCTTCCTGCAGAACCAACCTCATCCGCACGCTGCGGCCAGGCACCTTT 240

Qy. 81 GlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGly 100

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 3, 2005, 01:05:36 ; Search time 619 Seconds
(without alignments)
4016.626 Million cell updates/sec

Title: US-10-735-256-2
Perfect score: 2226
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....LSAGLPSPLLCLLLLVPDDL 420

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	No.	Score	Match Length DB ID				
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	6	2186	98.2	1865	8	AAD51236	Aad51236 Human REM
	7	2181	98.0	1976	12	ADM72161	Adm72161 Human NTR
	8	2177	97.8	2565	10	ADE06964	Ade06964 Novel cod
	9	2130	95.7	1263	8	ACC70357	Acc70357 Nucleotid
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	12	1822.5	81.9	1598	10	ADC13558	Adc13558 Human NOV
	13	1342.5	60.3	143899	6	AAL38336	Aal38336 Genomic s
	14	1291	58.0	791	6	ABK34490	Abk34490 Human cDN
	15	1281	57.5	1003	2	AAX30364	Aax30364 DNA encod
	16	1281	57.5	1003	10	ADB47736	Adb47736 Novel hum
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	19	948	42.6	1539	12	ADN12046	Adn12046 Novel hum
	20	946	42.5	1407	8	AAL55338	Aal55338 Rat NgRH2
	21	946	42.5	1480	12	ADN12048	Adn12048 Novel rat
c	22	921	41.4	215980	6	AAL38337	Aal38337 Complemen
	23	920.5	41.4	1383	6	AAL38334	Aal38334 Mouse NgR
	24	842	37.8	972	5	AAS79358	Aas79358 DNA encod
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	30	816.5	36.7	2236	2	AAZ34229	Aaz34229 Human PRO
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	33	816.5	36.7	2236	3	AAA77613	Aaa77613 Human PRO
	34	816.5	36.7	2236	3	AAA49724	Aaa49724 Human PRO
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	36	816.5	36.7	2236	5	AAC88958	Aac88958 Human PRO
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ALIGNMENTS

RESULT 1

AAL38333

ID AAL38333 standard; cDNA; 1260 BP.

XX

AC AAL38333;

XX

DT 15-AUG-2002 (first entry)

XX

DE Human NgR2 cDNA sequence derived from genomic sequence AC013606.

XX

KW Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;
KW NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury;
KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;
KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;
KW multifocal leukoencephalopathy; panencephalitis; Spongy degeneration;
KW Alexander's disease; Canavan's disease; metachromatic leukodystrophy;
KW Krabbe's disease; immune; bait protein; genetic mapping; gene therapy;
KW transgenic animal; unregulated cellular growth; cancer; tumour; human;
KW gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

1. .1260

FT

/*tag= a

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/product= "Protein of human NgR2"

FT

/note= "No stop codon"

FT

sig_peptide

1. .90

FT

/*tag= b

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PN WO200229059-A2.

XX

PD 11-APR-2002.

XX

PF 06-OCT-2001; 2001WO-US031488.

XX

PR 06-OCT-2000; 2000US-0238361P.

XX

PA (UYYA) UNIV YALE.

PA

(BIOJ) BIOGEN INC.

XX

PI Strittmatter SM, Cate RL, Sah DWY;

XX

DR WPI; 2002-416677/44.

DR

P-PSDB; AAO21477.

XX

PT Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for
PT treating central nervous system disorder, cerebral injury, spinal cord
PT injury, stroke, and demyelinating diseases.

XX

PS Example 2; Page 103; 277pp; English.

XX

CC The invention relates to a Nogo receptor homologue polypeptide, NgR2 or
 CC NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT
 CC sequence, or a 420, 461 or 392 amino acid sequence, all given in the
 CC specification. The NgR3 protein or its binding antibody is useful for
 CC decreasing inhibition of axonal growth of a central nervous system (CNS)
 CC neuron, by contacting the neuron NgR3 or its antibody, and for treating
 CC CNS disease, disorder or injury. NgR3 or a vector comprising NgR3 is
 CC useful for treating cerebral injury, spinal cord injury, stroke,
 CC demyelinating diseases, e.g. multiple sclerosis, monophasic
 CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
 CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration,
 CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy and
 CC Krabbe's disease. NgR3 is useful for inducing an immune response in a
 CC mammal against NgR3, as a bait protein in a two-hybrid or three-hybrid
 CC assay, and as a research tool for identification, characterisation and
 CC purification of interacting, regulatory proteins. The nucleotide
 CC sequences of the invention are useful for screening for RFLP associated
 CC with certain disorders, for genetic mapping, and for gene therapy. The
 CC vector containing NgR3 is useful for producing non-human transgenic
 CC animals. The NgR3 binding antibody is useful for isolating and purifying
 CC NgR3, for localisation and/or quantitation of NgR3, and for diagnostic
 CC and therapeutic purposes. The sequences of the invention, vectors and
 CC antibodies are useful for treating or preventing unregulated cellular
 CC growth such as cancer and tumour growth. This polynucleotide sequence
 CC represents the human NgR2 cDNA sequence derived from the genomic sequence
 CC AC013606 of the invention

XX

SQ Sequence 1260 BP; 170 A; 524 C; 364 G; 202 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.84e-129	Length:	1260
Score:	2226.00	Matches:	420
Percent Similarity:	100.00%	Conservative:	0
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US-10-735-256-2 (1-420) x AAL38333 (1-1260)

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Qy	21 LeuLeuAlaLeuProLeuAlaAlaProSerCysProMetLeuCysThrCysTyrSerSer	40
Db	61 CTCCTGGCCCTGCCCTGGCGGCCCCAGCTGCCCCATGCTCTGCACCTGCTACTCATCC	120
Qy	41 ProProThrValSerCysGlnAlaAsnAsnPheSerSerValProLeuSerLeuProPro	60
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Qy	61 SerThrGlnArgLeuPheLeuGlnAsnAsnLeuIleArgThrLeuArgProGlyThrPhe	80
Db	181 AGCACTCAGCGACTCTTCTGCGAACAACCTCATCCGACGCTGCGGCCAGGCACCTTT	240
Qy	81 GlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGly	100

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 3, 2005, 02:31:26 ; Search time 223 Seconds
(without alignments)
3081.777 Million cell updates/sec

Title: US-10-735-256-2
Perfect score: 2226
Sequence: 1 MLPGLRRLQLQAPASACLLLM.....LSAGLPSPLLCLLLLVPPhL 420

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	816.5	36.7	1422	4	US-09-949-016-2577	Sequence 2577, Ap
4	800.5	36.0	1777	4	US-09-461-325-40	Sequence 40, Appl
5	800.5	36.0	1777	4	US-10-012-542-40	Sequence 40, Appl
6	800.5	36.0	1777	4	US-10-115-123-40	Sequence 40, Appl
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9	380.5	17.1	2852	3	US-09-063-950-1	Sequence 1, Appli
10	377.5	17.0	9036	4	US-09-949-016-16866	Sequence 16866, A
11	374.5	16.8	2587	4	US-09-949-016-5124	Sequence 5124, Ap
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13	338	15.2	2341	4	US-09-520-781-9	Sequence 9, Appli
14	338	15.2	2607	4	US-09-520-781-11	Sequence 11, Appl
15	337.5	15.2	2906	4	US-09-907-794A-291	Sequence 291, App
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17	337.5	15.2	2906	4	US-09-902-775A-291	Sequence 291, App
18	337.5	15.2	2906	4	US-09-906-700-291	Sequence 291, App
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22	337.5	15.2	2906	4	US-09-905-381A-291	Sequence 291, App
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26	330.5	14.8	3679	4	US-09-907-794A-244	Sequence 244, App
27	330.5	14.8	3679	4	US-09-905-125A-244	Sequence 244, App
28	330.5	14.8	3679	4	US-09-902-775A-244	Sequence 244, App
29	330.5	14.8	3679	4	US-09-906-700-244	Sequence 244, App
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32	330.5	14.8	3679	4	US-09-909-064-244	Sequence 244, App
33	330.5	14.8	3679	4	US-09-905-381A-244	Sequence 244, App
34	330.5	14.8	3679	4	US-09-906-618-244	Sequence 244, App
35	328.5	14.8	2290	4	US-09-907-794A-72	Sequence 72, Appl
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44	328	14.7	7452	3	US-08-592-500-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 58, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (422)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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; LOCATION: (758)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-774-639-58
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Pred. No.:	4.26e-108	Length:	1003
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Percent Similarity:	96.31%	Conservative:	3
Best Local Similarity:	95.20%	Mismatches:	9
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US-10-735-256-2 (1-420) x US-09-774-639-58 (1-1003)

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Qy      60 oSerThrGlnArgLeuPheLeuGlnAsnAsnLeuIleArgThrLeuArgProGlyThrPh 80
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Qy      80 eGlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGl 100
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Run on: September 3, 2005, 02:41:31 ; Search time 728 Seconds
(without alignments)
3778.219 Million cell updates/sec

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Perfect score: 2226
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100
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Database : Published_Applications_NA:*
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 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2226	100.0	1260	10	US-09-972-546-1	Sequence 1, Appli
2	2226	100.0	1260	21	US-10-735-256-1	Sequence 1, Appli
3	2186	98.2	1865	21	US-10-477-714-43	Sequence 43, Appl
4	1822.5	81.9	1598	17	US-10-188-248-37	Sequence 37, Appl
5	1342.5	60.3	143899	10	US-09-972-546-15	Sequence 15, Appl
6	1342.5	60.3	143899	21	US-10-735-256-15	Sequence 15, Appl
7	1291	58.0	791	9	US-09-823-245A-259	Sequence 259, App
8	1281	57.5	1003	10	US-09-774-639-58	Sequence 58, Appl
9	1281	57.5	1003	10	US-09-969-730-19	Sequence 19, Appl
10	1281	57.5	1003	17	US-10-621-363-19	Sequence 19, Appl
11	948	42.6	1436	20	US-10-487-886-1	Sequence 1, Appli
12	946	42.5	1407	20	US-10-487-886-24	Sequence 24, Appl
c 13	921	41.4	215980	10	US-09-972-546-16	Sequence 16, Appl
c 14	921	41.4	215980	21	US-10-735-256-16	Sequence 16, Appl
15	920.5	41.4	1383	10	US-09-972-546-3	Sequence 3, Appli
16	920.5	41.4	1383	21	US-10-735-256-3	Sequence 3, Appli
17	837.5	37.6	1176	10	US-09-972-546-13	Sequence 13, Appl
18	837.5	37.6	1176	21	US-10-735-256-13	Sequence 13, Appl
19	816.5	36.7	1719	9	US-09-758-140-1	Sequence 1, Appli
20	816.5	36.7	1719	9	US-09-972-599A-1	Sequence 1, Appli
21	816.5	36.7	2138	20	US-10-723-860-6549	Sequence 6549, Ap
22	816.5	36.7	2236	9	US-09-978-295A-399	Sequence 399, App
23	816.5	36.7	2236	9	US-09-978-697-399	Sequence 399, App
24	816.5	36.7	2236	9	US-09-978-192A-399	Sequence 399, App
25	816.5	36.7	2236	9	US-09-999-832A-399	Sequence 399, App
26	816.5	36.7	2236	10	US-09-978-189-399	Sequence 399, App
27	816.5	36.7	2236	10	US-09-978-608A-399	Sequence 399, App
28	816.5	36.7	2236	10	US-09-978-585A-399	Sequence 399, App
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ALIGNMENTS

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; Sequence 1, Application US/09972546
; Publication No. US20030124704A1
; GENERAL INFORMATION:
;   APPLICANT: STRITTMATTER, STEPHEN M.
;   APPLICANT:  CATE, RICHARD L.
;   APPLICANT:  SAH, DINAH W.Y.
;   TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
;   FILE REFERENCE: A116US
;   CURRENT APPLICATION NUMBER: US/09/972,546
;   CURRENT FILING DATE: 2001-10-06
;   PRIOR APPLICATION NUMBER: 60/238,361
;   PRIOR FILING DATE: 2000-10-06
;   NUMBER OF SEQ ID NOS: 19
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1260
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-972-546-1

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Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

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Db	181	AGCACTCAGCGACTCTTCTGCAGAACAACTCATCCGCACGCTGCGGCCAGGCACCTTT	240
Qy	81	GlySerAsnLeuLeuThrLeuTrpLeuPheSerAsnAsnLeuSerThrIleTyrProGly	100
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Qy	101	ThrPheArgHisLeuGlnAlaLeuGluGluLeuAspLeuGlyAspAsnArgHisLeuArg	120
Db	301	ACTTTCCGCCACTTGCAAGCCCTGGAGGAGCTGGACCTCGGTGACAACCGGCACCTGCGC	360
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Qy	301	AlaLeuArgGluAlaAspPheGlnAlaCysProProAlaAlaProThrArgProGlySer	320
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RESULT 2

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; Sequence 1, Application US/10735256
; Publication No. US20050048520A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: CATE, RICHARD L.
; APPLICANT: SAH, DINAH W.Y.
; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
; FILE REFERENCE: A116 CON
; CURRENT APPLICATION NUMBER: US/10/735,256
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/972,546
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/238,361
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-735-256-1

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Alignment Scores:

Pred. No.:	1.16e-211	Length:	1260
Score:	2226.00	Matches:	420
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-10-735-256-2 (1-420) x US-10-735-256-1 (1-1260)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 3, 2005, 02:00:16 ; Search time 3358 Seconds
(without alignments)
4760.868 Million cell updates/sec

Title: US-10-735-256-2
Perfect score: 2226
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Searched: 34239544 seqs, 19032134700 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	31	699	31.4	557	7	CN264434		CN264434	170004243
	32	688	30.9	930	4	BI760526		BI760526	603045070
	33	684	30.7	1302	4	BM807465		BM807465	AGENCOURT
	34	673	30.2	385	6	CB702344		CB702344	AMGNNUC:S
	35	673	30.2	771	4	BG469747		BG469747	602534219
c	36	661.5	29.7	415	2	AW131579		AW131579	xf31f08.x
	37	659	29.6	367	2	BF940539		BF940539	nae21h02.
c	38	654	29.4	384	2	AW293195		AW293195	UI-H-BI2-
	39	652	29.3	907	5	BU540705		BU540705	AGENCOURT
	40	648	29.1	884	5	BX331981		BX331981	BX331981
	41	643.5	28.9	1052	5	BX461669		BX461669	BX461669
	42	640.5	28.8	953	5	BU500558		BU500558	AGENCOURT
	43	634	28.5	675	7	CK961565		CK961565	4075847 B
	44	594	26.7	544	6	CB612057		CB612057	AMGNNUC:N
c	45	591	26.5	1018	5	BX388350		BX388350	BX388350

ALIGNMENTS

RESULT 1

BU707423

LOCUS BU707423 751 bp mRNA linear EST 15-JUL-2003

DEFINITION UI-M-FR0-cap-e-04-0-UI.r1 NIH_BMAP_FR0 Mus musculus cDNA clone
IMAGE:6415467 5', mRNA sequence.

ACCESSION BU707423

VERSION BU707423.1 GI:23638879

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 751)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cdna Library preparation: Dr. M. Bento Soares, University of Iowa

cdna Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .751

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6415467"

/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_FR0"

/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is AGCGAGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

ORIGIN